

SEQ ID NO:	Clone	K _d , nM	K _i , nM
195	14N	0.4	2.0
199	25N	0.9	
191	4N	0.7	23.3
189	1N	0.5	16.7
205	36N	8.27	
203	34N	0.8	
207	42N	0.8	266.7
196	16N	1.4	
270	Consensus		

Summary Structure

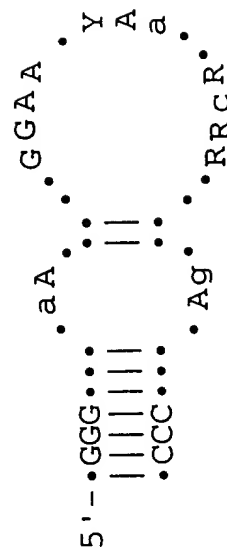


FIGURE 12C

Class 2

SEQ ID NO:	Clone	K _d , nM	K _i , nM	
209	47N	1.8		AGGAAGGUC <u>CAAGAGGAAA</u> CAGC
198	24N	1.2		<u>gacgaugcgg</u> GUGGGAAGA UGAG
202	29N	0.43	13.3	AGAAAGAAUGCA GGAAACAGCGAAA
204	35N	2.3		<u>ugcgggGCUUAG</u> GGAAA UGUU
192	6N	0.7	26.7	<u>acgaugcggc</u> AGGGAGCAA UGAACUCAAGUC <u>CGCGGUGCACGU</u> <u>GGGC</u>
190	2N	0.8	66.7	<u>GGCGA</u> AAGGAA CGAGA <u>gggaggacgaugcggCGGGAAGGUC</u>
211	54N	5.3		<u>GGG</u> GGAAG GAUU <u>UUGCCcagacgacucgcccga</u>
271		Consensus		<u>gggaggacgaugcggGAACCAACAG</u> CUCagacgacucgcccga

GUUcagacga gucgcccga
AAUGUGAC ACUGCGGca
Ccagacgac ucgcccga
Ucagacgac ucgcccga
agacgacuc gcccga
CGAA GACC |
AGCCCCCUGGUGGU |
ygay

Summary Structure

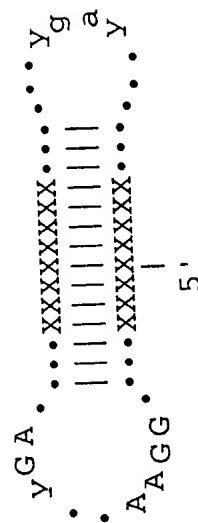


FIGURE 12D